```
=> fil reg; d que l2
FILE 'REGISTRY' ENTERED AT 16:06:40 ON 14 FEB 2006
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Property values tagged with IC are from the ZIC/VINITI data file
provided by InfoChem.

STRUCTURE FILE UPDATES:   13 FEB 2006  HIGHEST RN 874180-50-4
DICTIONARY FILE UPDATES:  13 FEB 2006  HIGHEST RN 874180-50-4

New CAS Information Use Policies, enter HELP USAGETERMS for details.

TSCA INFORMATION NOW CURRENT THROUGH JULY 14, 2005

  Please note that search-term pricing does apply when
  conducting SmartSELECT searches.

**********************************************************************
*                                                                    *
* The CA roles and document type information have been removed from *
* the IDE default display format and the ED field has been added,   *
* effective March 20, 2005.  A new display format, IDERL, is now    *
* available and contains the CA role and document type information. *
*                                                                    *
**********************************************************************

Structure search iteration limits have been increased.  See HELP SLIMITS
for details.

REGISTRY includes numerically searchable data for experimental and
predicted properties as well as tags indicating availability of
experimental property data in the original document.  For information
on property searching in REGISTRY, refer to:

http://www.cas.org/ONLINE/UG/regprops.html

L2             21 SEA FILE=REGISTRY ABB=ON  YDWRFNAF.Y|YDFRWNAF.Y|YDHFRWAF.Y/SQSF
                  P

=> d rn cn sql kwic nte lc 1-21 l2

L2   ANSWER 1 OF 21  REGISTRY  COPYRIGHT 2006 ACS on STN
RN   845849-93-67 REGISTRY
CN   TonB-dependent receptor (Porphyromonas gingivalis clone SW165 gene 0668)
     (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   226: PN: WO2005019249 SEQID: 226 claimed protein
SQL  757

SEQ    351 AYDMDYRALT ASLGTNYLFP NGLHTLSFDA VYDRFRFGYL YHDKDSSESL

HITS AT:  382-391

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**
LC   STN Files:   CA, CAPLUS, TOXCENTER
```

o = any amino acid
| = or

this search will retrieve both "D" & "L" forms of any of the amino acids in the seq.

1 family search done to allow for conservative substitution — see green tab

Use Registry # to match sequence to reference (References printed beginning on pg-8)

Sequence length =

L2 ANSWER 2 OF 21 REGISTRY COPYRIGHT 2006 ACS on STN
RN 811798-88-6 REGISTRY
CN L-Tyrosine, L-tyrosyl-L-α-aspartyl-D-phenylalanyl-L-arginyl-L-tryptophyl-L-asparaginyl-L-alanyl-L-phenylalanyl-3-aminoalanyl-, (2→9)-lactam (9CI) (CA INDEX NAME)
SQL 10

SEQ 1 YDFRWNAFXY
==========
HITS AT: 1-10

RELATED SEQUENCES AVAILABLE WITH SEQLINK
NTE

type	------ location ------		description
bridge	Asp-2	- Dpr-9	lactam
uncommon	Dpr-9	-	-
stereo	Phe-3	-	D

LC STN Files: CA, CAPLUS, USPATFULL

L2 ANSWER 3 OF 21 REGISTRY COPYRIGHT 2006 ACS on STN
RN 811798-86-4 REGISTRY
CN L-Tyrosine, L-tyrosyl-L-α-aspartyl-L-phenylalanyl-L-arginyl-L-tryptophyl-L-asparaginyl-L-alanyl-L-phenylalanyl-3-aminoalanyl-, (2→9)-lactam (9CI) (CA INDEX NAME)
SQL 10

SEQ 1 YDFRWNAFXY
==========
HITS AT: 1-10

RELATED SEQUENCES AVAILABLE WITH SEQLINK
NTE

type	------ location ------		description
bridge	Asp-2	- Dpr-9	lactam
uncommon	Dpr-9	-	-

LC STN Files: CA, CAPLUS, USPATFULL

L2 ANSWER 4 OF 21 REGISTRY COPYRIGHT 2006 ACS on STN
RN 811798-85-3 REGISTRY
CN L-Tyrosine, L-tyrosyl-L-α-aspartyl-L-tryptophyl-L-arginyl-D-phenylalanyl-L-asparaginyl-L-alanyl-L-phenylalanyl-3-aminoalanyl-, (2→9)-lactam (9CI) (CA INDEX NAME)
SQL 10

SEQ 1 YDWRFNAFXY
==========
HITS AT: 1-10

RELATED SEQUENCES AVAILABLE WITH SEQLINK
NTE

type	------ location ------		description
bridge	Asp-2	- Dpr-9	lactam

uncommon Dpr-9 - -
stereo Phe-5 - D

LC STN Files: CA, CAPLUS, USPATFULL

L2 ANSWER 5 OF 21 REGISTRY COPYRIGHT 2006 ACS on STN
RN 811798-83-1 REGISTRY
CN L-Tyrosine, L-tyrosyl-L-α-aspartyl-L-tryptophyl-L-arginyl-L-phenylalanyl-L-asparaginyl-L-alanyl-L-phenylalanyl-3-aminoalanyl-, (2→9)-lactam (9CI) (CA INDEX NAME)
SQL 10

SEQ 1 YDWRFNAFXY
==========
HITS AT: 1-10

RELATED SEQUENCES AVAILABLE WITH SEQLINK
NTE

---

type ------ location ------ description

---

bridge Asp-2 - Dpr-9 lactam
uncommon Dpr-9 - -

LC STN Files: CA, CAPLUS, USPATFULL

L2 ANSWER 6 OF 21 REGISTRY COPYRIGHT 2006 ACS on STN
RN 793505-90-5 REGISTRY
CN Protein (Azoarcus strain EbN1 590-amino acid) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank CAI09061
CN GenBank CAI09061 (Translated from: GenBank CR555306)
SQL 590

SEQ 201 NQINAIDLQK FHVPGTQLKE IFIPAQMISA SMDLTEQLGV EGYYQWRWNS
========
251 FKFDPSGTFF STVDVLGKGR RIAYVPTSII EDFAGPGACA DLPNGRCGDN
===
HITS AT: 244-253
LC STN Files: CA, CAPLUS, TOXCENTER

L2 ANSWER 7 OF 21 REGISTRY COPYRIGHT 2006 ACS on STN
RN 759392-75-1 REGISTRY
CN GenBank AAU94398 (9CI) (CA INDEX NAME) GenBank records printed at blue tab
OTHER NAMES:
CN GenBank AAU94398 (Translated from: GenBank BT015835)
SQL 299

SEQ 51 FNYKWEAFRF GIILAILTNL CITFSYHRNL THRSFKLPKW LEYPFAYSAL
==========
HITS AT: 51-60

RELATED SEQUENCES AVAILABLE WITH SEQLINK

L2 ANSWER 8 OF 21 REGISTRY COPYRIGHT 2006 ACS on STN
RN 704718-04-7 REGISTRY
CN Protein (Kluyveromyces lactis strain NRRL Y-1140 860-amino acid) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank CAG98599

CN GenBank CAG98599 (Translated from: GenBank CR382126)
SQL 860

SEQ 601 NLFKLTQPSY EFSIEQEQEI EILPGVPINI SIFNDFNKFK WGYFFKVKKL
=====
HITS AT: 636-645
LC STN Files: CA, CAPLUS

L2 ANSWER 9 OF 21 REGISTRY COPYRIGHT 2006 ACS on STN
RN 698962-52-6 REGISTRY
CN GenBank AAT47784 (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAT47784 (Translated from: GenBank BT014933)
SQL 299

SEQ 51 FNYKWEAFRF GIILAILTNL CITFSYHRNL THRSFKLPKW LEYPFAYSAL
==========
HITS AT: 51-60

RELATED SEQUENCES AVAILABLE WITH SEQLINK

L2 ANSWER 10 OF 21 REGISTRY COPYRIGHT 2006 ACS on STN
RN 681216-55-7 REGISTRY
CN L-Tyrosinamide, L-tyrosyl-L-α-aspartyl-D-phenylalanyl-L-arginyl-L-tryptophyl-L-asparaginyl-L-alanyl-L-phenylalanyl-3-amino-L-alanyl-, (2→9)-lactam (9CI) (CA INDEX NAME)
SQL 10

SEQ 1 YDFRWNAFXY
==========
HITS AT: 1-10

RELATED SEQUENCES AVAILABLE WITH SEQLINK
NTE modified

type	------ location ------		description
terminal mod.	Tyr-10	-	C-terminal amide
bridge	Asp-2	- Dpr-9	lactam
uncommon	Dpr-9	-	-
stereo	Phe-3	-	D

LC STN Files: CA, CAPLUS, CASREACT

L2 ANSWER 11 OF 21 REGISTRY COPYRIGHT 2006 ACS on STN
RN 681216-54-6 REGISTRY
CN L-Tyrosinamide, L-tyrosyl-L-α-aspartyl-L-phenylalanyl-L-arginyl-L-tryptophyl-L-asparaginyl-L-alanyl-L-phenylalanyl-3-amino-L-alanyl-, (2→9)-lactam (9CI) (CA INDEX NAME)
SQL 10

SEQ 1 YDFRWNAFXY
==========
HITS AT: 1-10

RELATED SEQUENCES AVAILABLE WITH SEQLINK
NTE modified

	------ location ------		description

terminal mod.	Tyr-10	-	C-terminal amide
bridge	Asp-2	- Dpr-9	lactam
uncommon	Dpr-9	-	-

LC STN Files: CA, CAPLUS, CASREACT

L2 ANSWER 12 OF 21 REGISTRY COPYRIGHT 2006 ACS on STN
RN 681216-53-5 REGISTRY
CN L-Tyrosinamide, L-tyrosyl-L-α-aspartyl-L-tryptophyl-L-arginyl-D-phenylalanyl-L-asparaginyl-L-alanyl-L-phenylalanyl-3-amino-L-alanyl-, (2→9)-lactam (9CI) (CA INDEX NAME)
SQL 10

SEQ 1 YDWRFNAFXY
HITS AT: 1-10

RELATED SEQUENCES AVAILABLE WITH SEQLINK
NTE modified

type	location		description
terminal mod.	Tyr-10	-	C-terminal amide
bridge	Asp-2	- Dpr-9	lactam
uncommon	Dpr-9	-	-
stereo	Phe-5	-	D

LC STN Files: CA, CAPLUS, CASREACT

L2 ANSWER 13 OF 21 REGISTRY COPYRIGHT 2006 ACS on STN
RN 681216-52-4 REGISTRY
CN L-Tyrosinamide, L-tyrosyl-L-α-aspartyl-L-tryptophyl-L-arginyl-L-phenylalanyl-L-asparaginyl-L-alanyl-L-phenylalanyl-3-amino-L-alanyl-, (2→9)-lactam (9CI) (CA INDEX NAME)
SQL 10

SEQ 1 YDWRFNAFXY
HITS AT: 1-10

RELATED SEQUENCES AVAILABLE WITH SEQLINK
NTE modified

type	location		description
terminal mod.	Tyr-10	-	C-terminal amide
bridge	Asp-2	- Dpr-9	lactam
uncommon	Dpr-9	-	-

LC STN Files: CA, CAPLUS, CASREACT

L2 ANSWER 14 OF 21 REGISTRY COPYRIGHT 2006 ACS on STN
RN 666517-17-5 REGISTRY
CN Transcription-associated protein (Glycine max clone PAT_MRT3847_141913C.1.pep fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1255: PN: US20040031072 SEQID: 189255 claimed protein
SQL 78

SEQ 1 GFSSSVWVPQ NFRNEREIST KNPNFWDFHE QGFIYLKIFL SGFCLFEIFT

```
                                   ===== =====
HITS AT:   26-35
LC   STN Files:   CA, CAPLUS

L2   ANSWER 15 OF 21  REGISTRY  COPYRIGHT 2006 ACS on STN
RN   579411-40-8  REGISTRY
CN   TonB-dependent receptor (Porphyromonas gingivalis strain W83 gene PG0668)
     (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   GenBank AAQ65844
CN   GenBank AAQ65844 (Translated from: GenBank AE017174)
SQL  757

SEQ    351 AYDMDYRALT ASLGTNYLFP NGLHTLSFDA VYDRFRFGYL YHDKDSSESL
                                              ========= =
HITS AT:   382-391

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**
LC   STN Files:   CA, CAPLUS, TOXCENTER

L2   ANSWER 16 OF 21  REGISTRY  COPYRIGHT 2006 ACS on STN
RN   508591-72-8  REGISTRY
CN   Protein (Bacteroides thetaiotaomicron strain VPI-5482 gene BT0315) (9CI)
     (CA INDEX NAME)
OTHER NAMES:
CN   GenBank AAO75422
CN   GenBank AAO75422 (Translated from: GenBank AE016927)
SQL  429

SEQ    151 AFPTFSNPLW WDWRYNSYGW GWNYGWGWNR PYYGWGYYPG SWGGWYGGYW
                      ==========
HITS AT:   161-170
LC   STN Files:   CA, CAPLUS

L2   ANSWER 17 OF 21  REGISTRY  COPYRIGHT 2006 ACS on STN
RN   405354-78-1  REGISTRY
CN   Protein PG13 (Porphyromonas gingivalis strain W50) (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   GenBank AAF81416
CN   GenBank AAF81416 (Translated from: GenBank AF237558)
SQL  757

SEQ    351 AYDMDYRALT ASLGTNYLFP NGLHTLSFDA VYDRFRFGYL YHDKDSSESL
                                              ========= =
HITS AT:   382-391

**RELATED SEQUENCES AVAILABLE WITH SEQLINK**
LC   STN Files:   CA, CAPLUS, TOXCENTER

L2   ANSWER 18 OF 21  REGISTRY  COPYRIGHT 2006 ACS on STN
RN   395121-90-1  REGISTRY
CN   Herbicide-target protein (Arabidopsis thaliana clone WO0210210-SEQID-83)
     (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   83: PN: WO0210210 SEQID: 83 claimed protein
SQL  299

SEQ     51 FNYKWEAFRF GIILAILTNL CITFSYHRNL THRSFKLPKW LEYPFAYSAL
           ==========
HITS AT:   51-60
```

RELATED SEQUENCES AVAILABLE WITH SEQLINK
LC STN Files: CA, CAPLUS

L2 ANSWER 19 OF 21 REGISTRY COPYRIGHT 2006 ACS on STN
RN 321763-44-4 REGISTRY
CN Protein (Arabidopsis thaliana clone T21E18 gene T21E18.15) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAF80133
CN GenBank AAF80133 (Translated from: GenBank AC024174)
SQL 299

SEQ 51 FNYKWEAFRF GIILAILTNL CITFSYHRNL THRSFKLPKW LEYPFAYSAL
(==========)
HITS AT: 51-60

RELATED SEQUENCES AVAILABLE WITH SEQLINK
LC STN Files: CA, CAPLUS

L2 ANSWER 20 OF 21 REGISTRY COPYRIGHT 2006 ACS on STN
RN 227093-10-9 REGISTRY
CN Protein PG13 (Porphyromonas gingivalis strain ATCC_53978 precursor) (9CI) (CA INDEX NAME)
SQL 757

SEQ 351 AYDMDYRALT ASLGTNYLFP NGLHTLSFDA VYDRFRFGYL YHDKDSSESL
(==========)
HITS AT: 382-391
LC STN Files: CA, CAPLUS, TOXCENTER, USPATFULL

L2 ANSWER 21 OF 21 REGISTRY COPYRIGHT 2006 ACS on STN
RN 226933-98-8 REGISTRY
CN Protein PG13 (Porphyromonas gingivalis strain ATCC_53978 open reading frame) (9CI) (CA INDEX NAME)
SQL 763

SEQ 351 TFSEKKAYDM DYRALTASLG TNYLFPNGLH TLSFDAVYDR FRFGYLYHDK
(==========)
HITS AT: 388-397
LC STN Files: CA, CAPLUS, TOXCENTER, USPATFULL

=> fil capl casrea uspatf toxcenter; s l2
FILE 'CAPLUS' ENTERED AT 16:07:35 ON 14 FEB 2006
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FILE 'USPATFULL' ENTERED AT 16:07:35 ON 14 FEB 2006
CA INDEXING COPYRIGHT (C) 2006 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'TOXCENTER' ENTERED AT 16:07:35 ON 14 FEB 2006
COPYRIGHT (C) 2006 ACS

Registry file answer set crossed into bibliographic files to get references

```
L4          22 L2

=> dup rem l4
PROCESSING COMPLETED FOR L4
L5          15 DUP REM L4 (7 DUPLICATES REMOVED)
               ANSWERS '1-13' FROM FILE CAPLUS
               ANSWERS '14-15' FROM FILE USPATFULL

=> d ibib ed abs hitrn 1-15; fil hom

L5   ANSWER 1 OF 15  CAPLUS  COPYRIGHT 2006 ACS on STN DUPLICATE 1
ACCESSION NUMBER:         2005:182692  CAPLUS
DOCUMENT NUMBER:          142:255838
TITLE:                    Porphyromonas gingivalis virulence polynucleotides for
                          diagnosis, treatment, and monitoring of periodontal
                          diseases
INVENTOR(S):              Progulske-Fox, Ann; Hillman, Jeffrey Daniel;
                          Handfield, Martin
PATENT ASSIGNEE(S):       University of Florida, USA
SOURCE:                   PCT Int. Appl., 73 pp.
                          CODEN: PIXXD2
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   1
PATENT INFORMATION:

     PATENT NO.           KIND   DATE        APPLICATION NO.         DATE
     ---------------      ----   --------    --------------------    --------
     WO 2005019249         A2    20050303    WO 2004-US25778         20040810
     WO 2005019249         C1    20050512
     WO 2005019249         A3    20050915
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH,
             CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD,
             GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,
             LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI,
             NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY,
             TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW
         RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM,
             AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK,
             EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE,
             SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE,
             SN, TD, TG
PRIORITY APPLN. INFO.:                       US 2003-495589P     P  20030815
                                             US 2004-915002      A  20040810

ED   Entered STN:  04 Mar 2005
AB   The invention provides compns. and methods for the detection of
     Porphyromonas gingivalis and for the treatment and prevention of diseases
     and infections caused by P. gingivalis.  Thus, the sequences of 168
     genomic nucleic acids encoding 186 immunogenic proteins from P. gingivalis
     are provided.
IT   845849-93-6  use Registry # to match reference to sequence
     RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic
     use); PRP (Properties); THU (Therapeutic use); ANST (Analytical study);
     BIOL (Biological study); USES (Uses)
        (amino acid sequence; Porphyromonas gingivalis virulence
        polynucleotides for diagnosis, treatment, and monitoring of periodontal
        diseases)

L5   ANSWER 2 OF 15  CAPLUS  COPYRIGHT 2006 ACS on STN DUPLICATE 2
ACCESSION NUMBER:         2005:10350  CAPLUS
```

DOCUMENT NUMBER: 142:170777
TITLE: The genome sequence of an anaerobic aromatic-degrading denitrifying bacterium, strain EbN1
AUTHOR(S): Rabus, Ralf; Kube, Michael; Heider, Johann; Beck, Alfred; Heitmann, Katja; Widdel, Friedrich; Reinhardt, Richard
CORPORATE SOURCE: Max Planck Institut fuer Marine Mikrobiologie, Bremen, 28359, Germany
SOURCE: Archives of Microbiology (2005), 183(1), 27-36
CODEN: AMICCW; ISSN: 0302-8933
PUBLISHER: Springer GmbH
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 06 Jan 2005
AB Recent research on microbial degradation of aromatic and other refractory compds.
in anoxic waters and soils has revealed that nitrate-reducing bacteria belonging to the Betaproteobacteria contribute substantially to this process. The first complete genome is presented of a metabolically versatile representative, strain EbN1, which metabolizes various aromatic compds., including hydrocarbons. A circular chromosome (4.3 Mb) and two plasmids (0.21 and 0.22 Mb) encode 4603 predicted proteins. Ten anaerobic and four aerobic aromatic degradation pathways were recognized, with the encoding
genes mostly forming clusters. The presence of paralogous gene clusters (e.g., for anaerobic phenylacetate oxidation), high sequence similarities to orthologs from other strains (e.g., for anaerobic phenol metabolism) and frequent mobile genetic elements (e.g., more than 200 genes for transposases) suggest high genome plasticity and extensive lateral gene transfer during metabolic evolution of strain EbN1. Metabolic versatility is also reflected by the presence of multiple respiratory complexes. A large number of regulators, including more than 30 two-component and several FNR-type regulators, indicate a finely tuned regulatory network able to respond to the fluctuating availability of organic substrates and electron acceptors in the environment. The absence of genes required for nitrogen fixation and specific interaction with plants separates strain EbN1 ecophysiol. from the closely related nitrogen-fixing plant symbionts of the Azoarcus cluster. Supplementary material on sequence and annotation are provided at the Web page http://www.micro-genomes.mpg.de/ebn1/. The genome and two plasmid sequences are deposited in GenBank/EMBL/DDBJ under accession nos. CR555306-CR555308.
IT 793505-90-5
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genome sequence of anaerobic aromatic-degrading denitrifying Azoarcus strain EbN1)
REFERENCE COUNT: 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 3 OF 15 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 3
ACCESSION NUMBER: 2004:1127149 CAPLUS
DOCUMENT NUMBER: 142:86686
TITLE: Melanocortin receptor templates, peptides, and therapeutic use
INVENTOR(S): Haskell-Luevano, Carrie
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 15 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2004260063	A1	20041223	US 2003-602394	20030623
WO 2005000877	A2	20050106	WO 2004-US20329	20040622
WO 2005000877	A3	20050811		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2003-602394 A 20030623
ED Entered STN: 24 Dec 2004
AB The invention provides chimeric peptides and templates containing a combination of antagonist and agonist endogenous ligand residues. In particular, the invention provides chimeric peptides and templates thereof based on melanocortin agonist peptides and Agouti-related protein (AGRP). The invention provides multifunctional chimeric peptides having specific bioactivity at melanocortin receptors and their use as drugs to treat various diseases and conditions.
IT **811798-83-1P 811798-85-3P 811798-86-4P**
811798-88-6P
RL: PAC (Pharmacological activity); PRP (Properties); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(melanocortin receptor templates, peptides, and therapeutic use)

L5 ANSWER 4 OF 15 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 4
ACCESSION NUMBER: 2004:231619 CAPLUS
DOCUMENT NUMBER: 140:350780
TITLE: Identification of Putative Agouti-Related Protein(87-132)-Melanocortin-4 Receptor Interactions by Homology Molecular Modeling and Validation Using Chimeric Peptide Ligands
AUTHOR(S): Wilczynski, Andrzej; Wang, Xiang S.; Joseph, Christine G.; Xiang, Zhimin; Bauzo, Rayna M.; Scott, Joseph W.; Sorensen, Nicholas B.; Shaw, Amanda M.; Millard, William J.; Richards, Nigel G.; Haskell-Luevano, Carrie
CORPORATE SOURCE: Department of Medicinal Chemistry, University of Florida, Gainesville, FL, 32610, USA
SOURCE: Journal of Medicinal Chemistry (2004), 47(9), 2194-2207
CODEN: JMCMAR; ISSN: 0022-2623
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
OTHER SOURCE(S): CASREACT 140:350780
ED Entered STN: 22 Mar 2004
AB Agouti-related protein (AGRP) is one of only two naturally known antagonists of G-protein-coupled receptors (GPCRs) identified to date. Specifically, AGRP antagonizes the brain melanocortin-3 and -4 receptors

involved in energy homeostasis. α-MSH is one of the known endogenous agonists for these melanocortin receptors. Insight into putative interactions between the antagonist AGRP amino acids with the melanocortin-4 receptor (MC4R) may be important for the design of unique ligands for the treatment of obesity related diseases and is currently lacking in the literature. A three-dimensional homol. mol. model of the mouse MC4 receptor complex with the hAGRP(87-132) ligand docked into the receptor has been developed to identify putative antagonist ligand-receptor interactions. Key putative AGRP-MC4R interactions include the Arg111 of hAGRP(87-132) interacting in a neg. charged pocket located in a cavity formed by transmembrane spanning (TM) helixes 1, 2, 3, and 7, capped by the acidic first extracellular loop (EL1) and specifically with the conserved melanocortin receptor residues mMC4R Glu92 (TM2), mMC4R Asp114 (TM3), and mMC4R Asp118 (TM3). Addnl., Phe112 and Phe113 of hAGRP(87-132) putatively interact with an aromatic hydrophobic pocket formed by the mMC4 receptor residues Phe176 (TM4), Phe193 (TM5), Phe253 (TM6), and Phe254 (TM6). To validate the AGRP-mMC4R model complex presented herein from a ligand perspective, we generated nine chimeric peptide ligands based on a modified antagonist template of the hAGRP(109-118) (Tyr-c[Asp-Arg-Phe-Phe-Asn-Ala-Phe-Dpr]-Tyr-NH2). In these chimeric ligands, the antagonist AGRP Arg-Phe-Phe residues were replaced by the melanocortin agonist His/D-Phe-Arg-Trp amino acids. These peptides resulted in agonist activity at the mouse melanocortin receptors (mMC1R and mMC3-5Rs). The most notable results include the identification of a novel subnanomolar melanocortin peptide template Tyr-c[Asp-His-DPhe-Arg-Trp-Asn-Ala-Phe-Dpr]-Tyr-NH2 that is equipotent to α-MSH at the mMC1, mMC3, and mMC5 receptors but is 30-fold more potent than α-MSH at the mMC4R. Addnl., these studies identified a new and novel >200-fold MC4R vs. MC3R selective peptide Tyr-c[Asp-D-Phe-Arg-Trp-Asn-Ala-Phe-Dpr]-Tyr-NH2 template. Furthermore, when the His-DPhe-Arg-Trp sequence is used to replace the hAGRP Arg-Phe-Phe residues in the "mini"-AGRP (hAGRP87-120, C105A) template, a potent nanomolar agonist resulted at the mMC1R and MC3-5Rs.

IT **681216-52-4P 681216-53-5P 681216-54-6P 681216-55-7P**
RL: BSU (Biological study, unclassified); SPN (Synthetic preparation); BIOL (Biological study); PREP (Preparation)
(identification of putative Agouti-related protein(87-132)-melanocortin-4 receptor interactions by homol. mol. modeling and validation using chimeric peptide ligands)

REFERENCE COUNT: 78 THERE ARE 78 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 5 OF 15 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 5
ACCESSION NUMBER: 2003:721753 CAPLUS
DOCUMENT NUMBER: 139:208599
TITLE: Complete genome sequence of the oral pathogenic bacterium Porphyromonas gingivalis strain W83
AUTHOR(S): Nelson, Karen E.; Fleischmann, Robert D.; DeBoy, Robert T.; Paulsen, Ian T.; Fouts, Derrick E.; Eisen, Jonathan A.; Daugherty, Sean C.; Dodson, Robert J.; Durkin, A. Scott; Gwinn, Michelle; Haft, Daniel H.; Kolonay, James F.; Nelson, William C.; Mason, Tanya; Tallon, Luke; Gray, Jessica; Granger, David; Tettelin, Herve; Dong, Hong; Galvin, Jamie L.; Duncan, Margaret J.; Dewhirst, Floyd E.; Fraser, Claire M.
CORPORATE SOURCE: The Institute for Genomic Research, Rockville, MD, 20850, USA
SOURCE: Journal of Bacteriology (2003), 185(18), 5591-5601
CODEN: JOBAAY; ISSN: 0021-9193

PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 15 Sep 2003
AB The complete 2,343,479-bp genome sequence of the gram-neg., pathogenic oral bacterium Porphyromonas gingivalis strain W83, a major contributor to periodontal disease, was determined Whole-genome comparative anal. with other available complete genome sequences confirms the close relationship between the Cytophaga-Flavobacteria-Bacteroides (CFB) phylum and the green-sulfur bacteria. Within the CFB phyla, the genomes most similar to that of P. gingivalis are those of Bacteroides thetaiotaomicron and B. fragilis. Outside of the CFB phyla the most similar genome to P. gingivalis is that of Chlorobium tepidum, supporting the previous phylogenetic studies that indicated that the Chlorobia and CFB phyla are related, albeit distantly. Genome anal. of strain W83 reveals a range of pathways and virulence determinants that relate to the novel biol. of this oral pathogen. Among these determinants are at least six putative hemagglutinin-like genes and 36 previously unidentified peptidases. Genome anal. also reveals that P. gingivalis can metabolize a range of amino acids and generate a number of metabolic end products that are toxic to the human host or human gingival tissue and contribute to the development of periodontal disease. The genome sequence is deposited in GenBank/EMBL/DDBJ with accession number AE015924, and in the RefSeq Genome database with accession number NC_002950.
IT **579411-40-8**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of the oral pathogenic bacterium Porphyromonas gingivalis strain W83)
REFERENCE COUNT: 74 THERE ARE 74 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 6 OF 15 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 6
ACCESSION NUMBER: 2001:520210 CAPLUS
DOCUMENT NUMBER: 136:277667
TITLE: Identification of vaccine candidate antigens from a genomic analysis of Porphyromonas gingivalis
AUTHOR(S): Ross, B. C.; Czajkowski, L.; Hocking, D.; Margetts, M.; Webb, E.; Rothel, L.; Patterson, M.; Agius, C.; Camuglia, S.; Reynolds, E.; Littlejohn, T.; Gaeta, B.; Ng, A.; Kuczek, E. S.; Mattick, J. S.; Gearing, D.; Barr, I. G.
CORPORATE SOURCE: Research and Development, CSL Ltd., Parkville, 3052, Australia
SOURCE: Vaccine (2001), 19(30), 4135-4142
CODEN: VACCDE; ISSN: 0264-410X
PUBLISHER: Elsevier Science Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 19 Jul 2001
AB Porphyromonas gingivalis is a key periodontal pathogen which has been implicated in the etiol. of chronic adult periodontitis. Our aim was to develop a protein based vaccine for the prevention and or treatment of this disease. The authors used a whole genome sequencing approach to identify potential vaccine candidates. From a genomic sequence, the authors selected 120 genes using a series of bioinformatics methods. The selected genes were cloned for expression in Escherichia coli and screened with P. gingivalis antisera before purification and testing in an animal model. Two of these recombinant proteins (PG32 and PG33) demonstrated significant protection in the animal model, while a number were reactive with various

antisera. This process allows the rapid identification of vaccine candidates from genomic data.

IT 405354-78-1
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; identification of vaccine candidate antigens from genomic anal. of Porphyromonas gingivalis)

REFERENCE COUNT: 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 7 OF 15 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 7

ACCESSION NUMBER: 1999:388302 CAPLUS
DOCUMENT NUMBER: 131:40571
TITLE: Porphyromonas gingivalis polypeptides and polynucleotides
INVENTOR(S): Ross, Bruce Carter; Barr, Ian George; Patterson, Michelle Anne; Agius, Catherine Therese; Rothel, Linda Joy; Margetts, Mai Brigid; Hocking, Dianna Margaret; Webb, Elizabeth Ann
PATENT ASSIGNEE(S): CSL Limited, Australia
SOURCE: PCT Int. Appl., 587 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9929870	A1	19990617	WO 1998-AU1023	19981210
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9916487	A1	19990628	AU 1999-16487	19981208
CA 2313823	AA	19990617	CA 1998-2313823	19981210
ZA 9811333	A	20000508	ZA 1998-11333	19981210
EP 1037999	A1	20000927	EP 1998-960880	19981210
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2001526035	T2	20011218	JP 2000-524441	19981210
NZ 504811	A	20031031	NZ 1998-504811	19981210
US 6444799	B1	20020903	US 1998-221017	19981223
US 2002172976	A1	20021121	US 2002-194163	20020711
PRIORITY APPLN. INFO.:			AU 1997-839 A	19971210
			AU 1997-1182 A	19971231
			AU 1998-1546 A	19980130
			AU 1998-2264 A	19980310
			AU 1998-2911 A	19980409
			AU 1998-3128 A	19980423
			AU 1998-3338 A	19980505
			AU 1998-3654 A	19980522
			AU 1998-4917 A	19980729
			AU 1998-4963 A	19980730
			AU 1998-5028 A	19980804

WO 1998-AU1023 W 19981210
US 1998-221017 A1 19981223

ED Entered STN: 23 Jun 1999
AB The present invention relates to isolated Porphyromonas gingivalis polynucleotide sequences which can be used for recombinant production of P. gingivalis polypeptides and to develop nucleotide probes specific for P. gingivalis. The DNA sequences were selected from a large number of P. gingivalis sequences according to their indicative potential as vaccine candidates. This intuitive step involved comparison of the deduced protein sequence from the P. gingivalis DNA sequences to the known protein sequence databases. Some of the characteristics used to select useful vaccine candidates include: the expected cellular location, such as outer membrane proteins or secreted proteins; particular functional activities of similar proteins such as those with an enzymic or proteolytic activity; proteins involved in essential metabolic pathways that when inactivated or blocked may be deleterious or lethal to the organism; proteins that might be expected to play a role in the pathogenesis of the organism; and proteins which are paralogs to proteins with proven vaccine efficacy. One hundred twenty-two open reading frames (ORFs) are provided, along with the deduced amino acid sequences of the complete ORFs and putative signal moieties.
IT **226933-98-8P 227093-10-9P**
RL: BOC (Biological occurrence); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); PUR (Purification or recovery); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)
(amino acid sequence; Porphyromonas gingivalis polypeptides and polynucleotides)
REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 8 OF 15 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2004:209221 CAPLUS
DOCUMENT NUMBER: 140:212094
TITLE: Soybean nucleic acids and encoded proteins associated with transcription in plants and their uses for plant improvement
INVENTOR(S): La Rosa, Thomas J.; Zhou, Yihua; Kovalic, David K.; Cao, Yongwei
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 15 pp., Cont.-in-part of U.S. Ser. No. 985,678, abandoned.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2004031072 A1		20040212	US 2003-XU424599	20030428
PRIORITY APPLN. INFO.:			US 1999-304517	19990506
			US 2001-2001/985678	20011105
			US 2003-2003/424599	20030428

ED Entered STN: 16 Mar 2004
AB This invention provides 142,842 polynucleotide sequences isolated from a cDNA library generated from Glycine maximum The open reading frame in each polynucleotide sequence is identified by a combination of predictive and homol.-based methods. Functions of polypeptides encoded by the polynucleotides sequences are determined using a hierarchical classification tool, termed FunCAT, for Functional Categories Annotation Tool. Sequences

useful for producing transgenic plants having improved biol. properties are identified from their FunCAT annotations. [This abstract record is one of 72 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **666517-17-5**
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; soybean nucleic acids and encoded proteins associated with transcription in plants and their uses for plant improvement)

L5 ANSWER 9 OF 15 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2004:87042 CAPLUS
DOCUMENT NUMBER: 141:237390
TITLE: Complete genome sequence of the oral pathogenic bacterium Porphyromonas gingivalis strain W83. [Erratum to document cited in CA139:208599]
AUTHOR(S): Nelson, Karen E.; Fleischmann, Robert D.; DeBoy, Robert T.; Paulsen, Ian T.; Fouts, Derrick E.; Eisen, Jonathan A.; Daugherty, Sean C.; Dodson, Robert J.; Durkin, A. Scott; Gwinn, Michelle; Haft, Daniel H.; Kolonay, James F.; Nelson, William c.; Mason, Tanya; Tallon, Luke; Gray, Jessica; Granger, David; Tettelin, Herve; Hong, Dong; Galvin, Jamie L.; Duncan, Margaret J.; Dewhirst, Floyd E.; Fraser, Claire M.
CORPORATE SOURCE: Inst. Genomic Research, Rockville, MD, 20850, USA
SOURCE: Journal of Bacteriology (2004), 186(2), 593
CODEN: JOBAAY; ISSN: 0021-9193
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 03 Feb 2004
AB On page 5600, Acknowledgments, the following sentence should be added: "The Bacteroides fragilis sequence data used in the comparative anal. were produced by the Microbial Sequencing Group at the Sanger Institute and can be obtained from ftp://ftp.sanger.ac.uk/pub/pathogens/bf/.".
IT **579411-40-8**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of oral pathogenic bacterium Porphyromonas gingivalis strain W83 (Erratum))

L5 ANSWER 10 OF 15 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2004:570556 CAPLUS
DOCUMENT NUMBER: 141:66036
TITLE: Genome evolution in yeasts
AUTHOR(S): Dujon, Bernard; Sherman, David; Fischer, Gilles; Durrens, Pascal; Casaregola, Serge; Lafontaine, Ingrid; de Montigny, Jacky; Marck, Christian; Neuveglise, Cecile; Talla, Emmanuel; Goffard, Nicolas; Frangeul, Lionel; Aigle, Michel; Anthouard, Veronique; Babour, Anna; Barbe, Valerie; Barnay, Stephanie; Blanchin, Sylvie; Beckerich, Jean-Marie; Beyne, Emmanuelle; Bleykasten, Claudine; Boisrame, Anita; Boyer, Jeanne; Cattolico, Laurence; Confanioleri, Fabrice; de Daruvar, Antoine; Despons, Laurence; Fabre, Emmanuelle; Fairhead, Cecile; Ferry-Dumazet, Helene; Groppi, Alexis; Hantraye, Florence; Hennequin, Christophe; Jauniaux, Nicolas; Joyet, Philippe;

Kachouri, Rym; Kerrest, Alix; Koszul, Romain; Lemaire, Marc; Lesur, Isabelle; Ma, Laurence; Muller, Heloise; Nicaud, Jean-Marc; Nikolski, Macha; Oztas, Sophie; Ozier-Kalogeropoulos, Odile; Pellenz, Stefan; Potier, Serge; Richard, Guy-Franck; Straub, Marie-Laure; Suleau, Audrey; Swennen, Dominique; Tekaia, Fredj; Wesolowski-Louvel, Micheline; Westhof, Eric; Wirth, Benedicte; Zeniou-Meyer, Maria; Zivanovic, Ivan; Bolotin-Fukuhara, Monique; Thierry, Agnes; Bouchier, Christiane; Caudron, Bernard; Scarpelli, Claude; Gaillardin, Claude; Weissenbach, Jean; Wincker, Patrick; Souciet, Jean-Luc

CORPORATE SOURCE: Unite de Genetique Moleculaire des Levures (URA and UFR 927 Universite Pierre et Marie Curie), Paris, 75724, Fr.

SOURCE: Nature (London, United Kingdom) (2004), 430(6995), 35-44
CODEN: NATUAS; ISSN: 0028-0836

PUBLISHER: Nature Publishing Group
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 18 Jul 2004

AB Identifying the mechanisms of eukaryotic genome evolution by comparative genomics is often complicated by the multiplicity of events that have taken place throughout the history of individual lineages, leaving only distorted and superimposed traces in the genome of each living organism. The hemiascomycete yeasts, with their compact genomes, similar lifestyle and distinct sexual and physiol. properties, provide a unique opportunity to explore such mechanisms. The complete, assembled genome sequences of four yeast species are presented, selected to represent a broad evolutionary range within a single eukaryotic phylum, that after anal. proved to be molecularly as diverse as the entire phylum of chordates. A total of .apprx.24,200 novel genes were identified, the translation products of which were classified together with Saccharomyces cerevisiae proteins into .apprx.4700 families, forming the basis for interspecific comparisons. Anal. of chromosome maps and genome redundancies reveal that the different yeast lineages have evolved through a marked interplay between several distinct mol. mechanisms, including tandem gene repeat formation, segmental duplication, a massive genome duplication and extensive gene loss. The genome sequence are deposited in GenBank/EMBL/DDBJ under accession nos. CR380947-CR380959 for C. glabrata, CR382121-CR382126 for K. lactis, CR382127-CR382132 for Y. lipolytica, and CR382133-CR382139 for D. hansenii. [This abstract record is one of four records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **704718-04-7**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; genome evolution in yeasts based on complete genome sequences from Candida glabrata, Kluyveromyces lactis, Yarrowia lipolytica, and Debaryomyces hansenii)

L5 ANSWER 11 OF 15 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2003:234123 CAPLUS
DOCUMENT NUMBER: 138:363600
TITLE: A genomic view of the human-Bacteroides thetaiotaomicron symbiosis
AUTHOR(S): Xu, Jian; Bjursell, Magnus K.; Himrod, Jason; Deng, Su; Carmichael, Lynn K.; Chiang, Herbert C.; Hooper, Lora V.; Gordon, Jeffrey I.

CORPORATE SOURCE: Department of Molecular Biology and Pharmacology, Washington University School of Medicine, St. Louis, MO, 63110, USA
SOURCE: Science (Washington, DC, United States) (2003), 299(5615), 2074-2076
CODEN: SCIEAS; ISSN: 0036-8075
PUBLISHER: American Association for the Advancement of Science
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 26 Mar 2003
AB The human gut is colonized with a vast community of indigenous microorganisms that help shape our biol. The complete genome sequence is now presented for the Gram-neg. anaerobe Bacteroides thetaiotaomicron, a dominant member of our normal distal intestinal microbiota. Its 4779-member proteome includes an elaborate apparatus for acquiring and hydrolyzing otherwise indigestible dietary polysaccharides and an associated environment-sensing system consisting of a large repertoire of extracytoplasmic function sigma factors and one- and two-component signal transduction systems. These and other expanded paralogous groups shed light on the mol. mechanisms underlying symbiotic host-bacterial relationships in our intestine. The genome sequence is deposited in GenBank/EMBL/DDBJ under accession number AE015928 and in the RefSeq database under accession number NC_004663.
IT 508591-72-8
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of Bacteroides thetaiotaomicron and a genomic view of human-B. thetaiotaomicron symbiosis)
REFERENCE COUNT: 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 12 OF 15 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2002:107386 CAPLUS
DOCUMENT NUMBER: 136:146508
TITLE: Polypeptide targets for identifying new herbicidally active compounds based on sequence homology screening with Arabidopsis proteins
INVENTOR(S): Tietjen, Klaus; Weidler, Marcus
PATENT ASSIGNEE(S): Bayer Aktiengesellschaft, Germany
SOURCE: PCT Int. Appl., 261 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002010210	A2	20020207	WO 2001-EP9892	20010828
WO 2002010210	A3	20030220		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: WO 2001-EP9892 20010828
ED Entered STN: 10 Feb 2002
AB The invention relates to a method of identifying plant-specific polypeptides and nucleic acids encoding them which are suitable as sites of action for finding herbicides, to the use of the polypeptides identified for identifying new, herbicidally active compds., and methods of finding modulators of these polypeptides. All proteins encoded by the Arabidopsis thaliana genome (from TAIR and GenBank) are compared by sequence alignment to all other sequences which are accessible in the public database sequences (SwissProt and TrEMBL). A database comprising 3227 putative herbicide targets is identified by screening for a selected level of sequence similarity (expect-value or "E-value") and assigned biol. relevant properties (annotation). All the enzymes, receptors, and channels or transporters with the desired plant-specific E-values are filtered out from the annotations of the database according to the invention with the aid of a suitable algorithm with suitable search terms. Likewise, the invention relates to the use of the polypeptides in assay methods for identifying herbicidally active compds., including descriptions of activity assays, binding assays, displacement assays, scintillation proximity assays, two-hybrid systems, and calcium imaging or signaling assays.
IT **395121-90-1**
RL: AGR (Agricultural use); ANT (Analyte); ARU (Analytical role, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(amino acid sequence; polypeptide targets for identifying new herbicidally active compds. based on sequence homol. screening with Arabidopsis proteins)

L5 ANSWER 13 OF 15 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2001:13202 CAPLUS
DOCUMENT NUMBER: 134:142622
TITLE: Sequence and analysis of chromosome 1 of the plant Arabidopsis thaliana
AUTHOR(S): Theologis, Athanasios; Ecker, Joseph R.; Palm, Curtis J.; Federspiel, Nancy A.; Kaul, Samir; White, Owen; Alonso, Jose; Altafi, Hootan; Araujo, Rina; Bowman, Cheryl L.; Brooks, Shelise Y.; Buehler, Eugen; Chan, April; Chao, Qimin; Chen, Huaming; Cheuk, Rosa F.; Chin, Christina W.; Chung, Mike K.; Conn, Lane; Conway, Aaron B.; Conway, Andrew R.; Creasy, Todd H.; Dewar, Ken; Dunn, Patrick; Etgu, Pelin; Feldblyum, Tamara V.; Feng, JiDong; Fong, Betty; Fujii, Claire Y.; Gill, John E.; Goldsmith, Andrew D.; Haas, Brian; Hansen, Nancy F.; Hughes, Beth; Hulzar, Lucas; Hunter, Jonathan L.; Jenkins, Jennifer; Johnson-Hopson, Chanda; Khan, Shehnaz; Kahykin, Elizabeth; Kim, Christopher J.; Koo, Hean L.; Kremenetskala, Irina; Kurtz, David B.; Dwan, Andrea; Lam, Bao; Langin-Hooper, Stephane; Lee, Andrew; Lee, Jeong M.; Lenz, Catherine A.; Li, Joycelyn H.; Li, YaPing; Lin, Xiaoying; Liu, Shirley X.; Liu, Zhaoying A.; Luros, Jason S.; Maiti, Rama; Marziali, Andre; Militscher, Jennifer; Miranda, Molly; Nguyen, Michelle; Nierman, William C.; Osborne, Brian I.; Pai, Grace; Peterson, Jeremy; Pham, Paul K.; Rizzo, Michael; Rooney, Timothy; Rowley, Don; Sakano, Hitomi; Salzberg, Steven L.; Schwartz, Jody R.; Shinn, Paul; Southwick, Audrey M.; Sun, Hui; Tallon, Luke J.; Tambunga, Gabriel; Toriumi, Mitsue J.; Town, Christopher D.; Utterback,

Teresa; Van Aken, Susan; Vaysberg, Maria; Vysotskala, Valentina S.; Walker, Michelle; Wu, Dongying; Yu, Guixia; Fraser, Claire M.; Venter, J. Craig; David, Ronald W.
CORPORATE SOURCE: Plant Gene Expression Center/USDA-U.C., Albany, CA, 94710, USA
SOURCE: Nature (London) (2000), 408(6814), 816-820
CODEN: NATUAS; ISSN: 0028-0836
PUBLISHER: Nature Publishing Group
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 08 Jan 2001
AB The genome of the flowering plant Arabidopsis thaliana has five chromosomes. Here we report the sequence of the largest, chromosome 1, in two contigs of around 14.2 and 14.6 megabases. The contigs extend from the telomeres to the centromeric borders, regions rich in transposons, retrotransposons, and repetitive elements such as the 180-bp repeat. The chromosome represents 25% of the genome and contains about 6850 open reading frames, 236 tRNAs (tRNAs), and 12 small nuclear RNAs. There are 2 clusters of tRNA genes at different places on the chromosome. One consists of 27 tRNAPro genes and the other contains 27 tandem repeats of tRNATyr-tRNATyr-tRNASer genes. Chromosome 1 contains about 300 gene families with clustered duplications. There are also many repeat elements, representing 8% of the sequence. The GenBank Accession Nos. for chromosome 1 are AE005172 (northern arm) and AE005173 (southern arm). [This abstract record is one of two records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].
IT **321763-44-4**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; sequence and anal. of chromosome 1 of the plant Arabidopsis thaliana)
REFERENCE COUNT: 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 14 OF 15 USPATFULL on STN
ACCESSION NUMBER: 2002:307853 USPATFULL
TITLE: P. gingivalis polynucleotides and uses thereof
INVENTOR(S): Ross, Bruce Carter, Coburg, AUSTRALIA

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2002172976	A1	20021121
APPLICATION INFO.:	US 2002-194163	A1	20020711 (10)

RELATED APPLN. INFO.: Continuation of Ser. No. US 1998-221017, filed on 23 Dec 1998, GRANTED, Pat. No. US 6444799
Continuation-in-part of Ser. No. WO 1998-AU1023, filed on 10 Dec 1998, UNKNOWN

PRIORITY INFORMATION:	NUMBER	DATE
	AU 1997-1182	19971231
	AU 1998-1546	19980130
	AU 1998-2911	19980409
	AU 1998-3654	19980522
	WO 1998-AU1023	19981210

DOCUMENT TYPE: Utility
FILE SEGMENT: APPLICATION
LEGAL REPRESENTATIVE: Shantanu Basu, Morrison & Foerster LLP, 755 Page Mill

Road, Palo Alto, CA, 94304-1018
NUMBER OF CLAIMS: 25
EXEMPLARY CLAIM: 1
LINE COUNT: 533
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to isolated Porphorymonas gingivalis polynucleotides. The polynucleotides comprises a contiguous sequence of at least 20 nucleotides which is identical to a contiguous sequence of at least 20 nucleotides within a sequence selected from the group consisting of SEQ. ID. NO. 1 to SEQ. ID. NO. 1120 and sequences complementary thereto.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
IT **226933-98-8P 227093-10-9P**
(amino acid sequence; Porphyromonas gingivalis polypeptides and polynucleotides)

L5 ANSWER 15 OF 15 USPATFULL on STN
ACCESSION NUMBER: 2002:224711 USPATFULL
TITLE: P. gingivalis polynucleotides and uses thereof
INVENTOR(S): Ross, Bruce Carter, Victoria, AUSTRALIA
PATENT ASSIGNEE(S): CSL Limited, Parkville, AUSTRALIA (non-U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 6444799	B1	20020903	
APPLICATION INFO.:	US 1998-221017		19981223	(9)

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PRIORITY INFORMATION:	AU 1997-1182	19971231
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DOCUMENT TYPE: Utility
FILE SEGMENT: GRANTED
PRIMARY EXAMINER: Zeman, Mary K.
LEGAL REPRESENTATIVE: Morrison & Foerster LLP
NUMBER OF CLAIMS: 17
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 0 Drawing Figure(s); 0 Drawing Page(s)
LINE COUNT: 512
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to isolated Porphorymonas gingivalis polynucleotides. The polynucleotides comprises a contiguous sequence of at least 20 nucleotides which is identical to a contiguous sequence of at least 20 nucleotides within a sequence selected from the group consisting of SEQ. ID. NO. 1 to SEQ. ID. NO. 1120 and sequences complementary thereto.

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IT **226933-98-8P 227093-10-9P**
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